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Monte Carlo Simulations of Chromosome Aberrations: Comparing to Cytogenetic Data

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A Monte Carlo program was developed, based on the "classic" breakage-and-reunion model, for radiation-induced chromosomal aberrations. Proximity effects due to localization of chromosomes and limited range for break-break interactions in space and time are included. Only two adjustable parameters were used, with one corresponding to the total radiation dose. The other determines proximity effects by specifying the number of "interaction sites" in the cell nucleus. A very broad spectrum of published data was modelled: recent FISH results for 3-color chromosome painting and for 2-color painting with a total centromere probe; extensive data on the statistical distribution of dicentrics per cell; extensive data on the ratio of dicentrics to centric rings; and a dicentric dose-response curve. For any scoring, the analysis allows systematic extrapolation from observed damage to whole-genome damage, taking the actual arm-lengths of all chromosomes into account. With 12 interaction sites in the human cell nucleus, agreement between the experiments and the simulations was almost always within a factor of 2 or better, even when quite detailed categories of damage were scored. Monte Carlo methods adequately account for proximity effects, and give good quantitative estimates, with a minimum of adjustable parameters or theoretical assumptions.

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